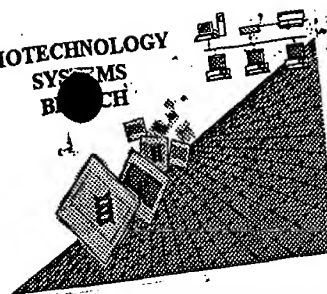# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/889,686_

Source: _Pur/09_

Date Processed by STIC: _7/27/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/889,686_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length.

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7____Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>

Sequence(s) _2_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 07/27/2001
PATENT APPLICATION: US/09/889,686   TIME: 19:30:20

Input Set : D:\03528.0133.PCUS00.txt   **Does Not Comply**
Output Set: N:\CRF3\07272001\I889686.raw   **Corrected Diskette Needed**

```
 4 <110> APPLICANT: DURING, Klaus
 5         BULOW, Lorenz
 7 <120> TITLE OF INVENTION: METHOD FOR THE CONTROLLED POST-HARVEST
 8         PRODUCTION OF PROTEINS IN HOST ORGANISMS
11 <130> FILE REFERENCE: 03528.0133.PCUS00
13 <140> CURRENT APPLICATION NUMBER: US/09/889,686
14 <141> CURRENT FILING DATE: 2001-07-27
16 <150> PRIOR APPLICATION NUMBER: PCT/DE00/03119
17 <151> PRIOR FILING DATE: 2000-09-05
19 <160> NUMBER OF SEQ ID NOS: 6
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 33
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Primer
31 <400> SEQUENCE: 1
32 catgtcaaca cataaggaag aagaggtaga aag                          33
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 35
36 <212> TYPE: DNA
37 <213> ORGANISM: Artifical sequence
39 <220> FEATURE:
39 <223> OTHER INFORMATION:
39 <400> SEQUENCE: 2
40 catgccatgg atcgatgacg gggttggcga gtgtg                        35
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 35
44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
47 <220> FEATURE:
48 <223> OTHER INFORMATION: Primer
50 <400> SEQUENCE: 3
51 catgccatgc cacaatttga tatattatgt aaaac                        35
53 <210> SEQ ID NO: 4
54 <211> LENGTH: 32
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Primer
61 <400> SEQUENCE: 4
62 gctctagatc agactgtggc agggaaaccc tc                           32
64 <210> SEQ ID NO: 5
65 <211> LENGTH: 36
66 <212> TYPE: DNA
67 <213> ORGANISM: Synthetic
```

Artifical ← C

see item 11 on Eva Summary Sheet

see item 10 on Eva Summary Sheet

RAW SEQUENCE LISTING   DATE: 07/27/2001
PATENT APPLICATION: **US/09/889,686**   TIME: 19:30:20

Input Set : **D:\03528.0133.PCUS00.txt**
Output Set: **N:\CRF3\07272001\I889686.raw**

```
69 <400> SEQUENCE: 5
70 ccatgccatg ccacaatttg atatattatg taaaac                        36
72 <210> SEQ ID NO: 6
73 <211> LENGTH: 32
74 <212> TYPE: DNA
75 <213> ORGANISM: Synthetic
77 <400> SEQUENCE: 6
78 gctctagatc agactgtggc agggaaaccc tc                            32
```

VERIFICATION SUMMARY   DATE: 07/27/2001
PATENT APPLICATION: **US/09/889,686**   TIME: 19:30:21

Input Set : **D:\03528.0133.PCUS00.txt**
Output Set: **N:\CRF3\07272001\I889686.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:39 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:39 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: